

HUMAN TRANSPORT PROTEINS

TECHNICAL FIELD

5 This invention relates to nucleic acid and amino acid sequences of human transport proteins and to the use of these sequences in the diagnosis, treatment, and prevention of transport, metabolic, neurological, cardiovascular, reproductive, and immune disorders, and cell proliferative disorders including cancer.

10 BACKGROUND OF THE INVENTION

 Eukaryotic cells are surrounded and subdivided into functionally distinct organelles by hydrophobic lipid bilayer membranes. These membranes act as a barrier to most molecules, and maintain the essential differences between the cytosol, the extracellular environment, and the contents of each intracellular organelle. Transport of essential nutrients, certain metal ions, metabolic waste
15 products, cell signaling molecules, macromolecules, and proteins across lipid membranes and between organelles must be mediated by a variety of transport molecules. Transport between the cytoplasm and the extracellular environment, and between the cytoplasm and luminal spaces of cellular organelles requires specific transport proteins. Each transport protein carries a particular class of molecule, such as ions, sugars, or amino acids, and often is specific to a certain molecular
20 species of the class.

 Cells and organelles require transport molecules to import and export essential nutrients and metal ions including K^+ , NH_4^+ , P_i , SO_4^{2-} , sugars, and vitamins, as well as various metabolic waste products. Transport proteins also play roles in antibiotic resistance, toxin secretion, ion balance, synaptic neurotransmission, kidney function, intestinal absorption, tumor growth, and other diverse
25 cell functions (Griffith, J. and C. Sansom (1998) The Transporter Facts Book, Academic Press, San Diego CA, pp. 3-29). Transport can occur by a passive concentration-dependent mechanism, or can be linked to an energy source such as ATP hydrolysis or an ion gradient. Proteins that function in transport include carrier proteins, which bind to a specific solute and undergo a conformational change that transfers the bound solute across the membrane, and channel proteins, which form
30 hydrophilic pores that allow specific solutes to diffuse through the membrane down an electrochemical solute gradient.

 Transport proteins are often multi-pass transmembrane proteins, which either actively transport molecules across the membrane or passively allow them to cross. Active transport involves directional pumping of a solute across the membrane, usually against an electrochemical gradient.
35 Active transport is tightly coupled to a source of metabolic energy, such as ATP hydrolysis or an electrochemically favorable ion gradient. Passive transport involves the movement of a solute down

its electrochemical gradient. Transport proteins can be further classified as either carrier proteins or channel proteins. Carrier proteins, which can function in active or passive transport, bind to a specific solute to be transported and undergo a conformational change which transfers the bound solute across the membrane. Channel proteins, which only function in passive transport, form hydrophilic pores across the membrane. When the pores open, specific solutes, such as inorganic ions, pass through the membrane and down the electrochemical gradient of the solute. Examples include facilitative transporters, the secondary active symporters and antiporters driven by ion gradients, and active ATP binding cassette transporters involved in multiple-drug resistance and targeting of antigenic peptides to MHC Class I molecules. Transported substrates range from nutrients and ions to a broad variety of drugs, peptides and proteins.

Information on the action of ARL-6 (ADP-ribosylation like factor), an endoplasmic reticulum transmembrane protein, can be found in Greenfield, J.J. and S. High (1999; J. Cell Sci. 112:1477-1486). Information on reduced folate carrier transporter proteins can be found in Dixon, K.H. et al. (1994; J. Biol. Chem. 269:17-20) and Moscow, J.A. et al. (1995; Cancer Res. 55:5983-5987).

Carrier proteins which transport a single solute from one side of the membrane to the other are called uniporters. In contrast, coupled transporters link the transfer of one solute with simultaneous or sequential transfer of a second solute, either in the same direction (symport) or in the opposite direction (antiport). For example, intestinal and kidney epithelia contain a variety of symporter systems driven by the sodium gradient that exists across the plasma membrane. Sodium moves into the cell down its electrochemical gradient and brings the solute into the cell with it. The sodium gradient that provides the driving force for solute uptake is maintained by the ubiquitous Na^+/K^+ ATPase. Sodium-coupled transporters include the mammalian glucose transporter (SGLT1), iodide transporter (NIS), and multivitamin transporter (SMVT). All three transporters have twelve putative transmembrane segments, extracellular glycosylation sites, and cytoplasmically-oriented N- and C-termini.

Mitochondrial carrier proteins are transmembrane-spanning proteins which transport ions and charged metabolites between the cytosol and the mitochondrial matrix. Examples include the ADP, ATP carrier protein; the 2-oxoglutarate/malate carrier; the phosphate carrier protein; the brown fat uncoupling protein which transports protons from the cytosol into the matrix; the pyruvate carrier; the dicarboxylate carrier which transports malate, succinate, fumarate, and phosphate; the tricarboxylate carrier which transports citrate and malate; and the Grave's disease carrier protein, a protein recognized by IgG in patients with active Grave's disease, an autoimmune disorder resulting in hyperthyroidism (Stryer, L. (1995) Biochemistry, W.H. Freeman and Company, New York NY, p. 551; PROSITE PDOC00189 Mitochondrial energy transfer proteins signature; Online Mendelian Inheritance in Man (OMIM) *275000 Graves Disease).

This class of transporters also includes the mitochondrial uncoupling proteins, which create

proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. The result is energy dissipation in the form of heat. Mitochondrial uncoupling proteins have been implicated as modulators of thermoregulation and metabolic rate, and have been proposed as potential targets for drugs against metabolic diseases such as obesity (Ricquier, D. et al. (1999) *J. Int. Med.* 245:637-642).

A number of metal ions such as iron, zinc, copper, cobalt, manganese, molybdenum, selenium, nickel, and chromium are important as cofactors for a number of enzymes. For example, zinc is required for the function of enzymes such as the extracellular matrix metalloproteinases, and zinc ions stabilize several motifs commonly found in transcription factors, including zinc fingers, zinc clusters, and LIM domains. Zinc and other metal ions must be provided in the diet, and are absorbed by transporters in the gastrointestinal tract. Plasma proteins transport the metal ions to the liver and other target organs, where specific transporters move the ions into cells and cellular organelles as needed. Imbalances in metal ion metabolism have been associated with a number of disease states (Danks, D.M. (1986) *J. Med. Genet.* 23:99-106).

The largest and most diverse family of transport proteins known are the ATP-binding cassette (ABC) transporters. As a family, ABC transporters can transport substances that differ markedly in chemical structure and size, ranging from small molecules such as ions, sugars, amino acids, peptides, and phospholipids, to lipopeptides, large proteins, and complex hydrophobic drugs. ABC proteins consist of four modules: two nucleotide-binding domains (NBD), which hydrolyze ATP to supply the energy required for transport, and two membrane-spanning domains (MSD), each containing six putative transmembrane segments. These four modules may be encoded by a single gene, as is the case for the cystic fibrosis transmembrane regulator (CFTR), or by separate genes. When encoded by separate genes, each gene product contains a single NBD and MSD. These "half-molecules" form homo- and heterodimers, such as Tap1 and Tap2, the endoplasmic reticulum-based major histocompatibility (MHC) peptide transport system. Several genetic diseases are attributed to defects in ABC transporters, such as the following diseases and their corresponding proteins: cystic fibrosis (CFTR, an ion channel), adrenoleukodystrophy (adrenoleukodystrophy protein, ALDP), Zellweger syndrome (peroxisomal membrane protein-70, PMP70), and hyperinsulinemic hypoglycemia (sulfonylurea receptor, SUR). Overexpression of the multidrug resistance (MDR) protein, another ABC transporter, in human cancer cells makes the cells resistant to a variety of cytotoxic drugs used in chemotherapy (Taglicht, D. and S. Michaelis (1998) *Methods Enzymol.* 292:131-163).

The nuclear pore complex (NPC) is a large multiprotein complex spanning the nuclear envelope which mediates the transport of proteins and RNA molecules between the nucleus and the cytoplasm, thus contributing to the regulation of gene expression. The NPC allows passive diffusion of ions, small molecules, and macromolecules under about 60kD, while larger macromolecules are transported by facilitated, energy-dependent pathways. Nuclear localization signals (NLS), consisting

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of short stretches of amino acids enriched in basic residues, are found on proteins that are targeted to the nucleus, such as the glucocorticoid receptor. The NLS is recognized by the NLS receptor, importin, which then interacts with the monomeric GTP-binding protein Ran. This NLS protein/receptor/Ran complex navigates the nuclear pore with the help of the homodimeric protein nuclear transport factor 2 (NTF2) (Nakielnny, S. and G. Dreyfuss (1997) *Curr. Opin. Cell Biol.* 9:420-429; Gorlich, D. (1997) *Curr. Opin. Cell Biol.* 9:412-419). Four O-linked glycoproteins, p62, p58, p54, and p45, exist as a stable "p62 complex" that forms a ring localized on both nucleoplasmic and cytoplasmic surfaces of the NPC. The p62, p58, and p54 proteins all interact directly with the cytosolic transport factors p97 and NTF2, suggesting that the p62 complex is an important ligand binding site near the central gated channel of the NPC (Hu, T. et al. (1996) *J. Cell Biol.* 134:589-601).

Transport can also occur through intercellular bridges which connect the cytoplasms of sister cells, for example in the male and female germline of species ranging from fruit flies to humans. These bridges allow passage of cytoplasmic materials between cells during development. Intercellular bridges have also been found to connect somatic cells. The nurse cells and oocyte of a *Drosophila* egg chamber, which are derived from a single precursor cell through four rounds of mitosis, are connected to each other through intercellular bridges called ring canals. The cells do not completely separate after mitosis; the mitotic cleavage furrows are transformed into ring canals by the addition of an actin cytoskeleton lining the tunnels between the cells. The *Drosophila* kelch protein functions in organizing actin in the ring canal. Mutations in kelch cause female sterility in *Drosophila*. Kelch contains four protein domains: the NTR domain at the N-terminus, the BTB or POZ domain, the IVR or intervening region; and the kelch repeat domain, which contains six 50-amino acid kelch repeats. The BTB or POZ domain, a 120-amino acid motif that is also found in several zinc-finger containing transcription factors, may be important in dimerization of kelch. Kelch repeats are found in other proteins as well and may be important for actin binding (Robinson, D.N. and L. Cooley (1997) *J. Cell Biol.* 138:799-810; Cooley, L. (1998) *Cell* 93:913-915).

Ion Channels

The electrical potential of a cell is generated and maintained by controlling the movement of ions across the plasma membrane. The movement of ions requires ion channels, which form an ion-selective pore within the membrane. Ion channels share common structural and mechanistic themes. The channel consists of four or five subunits or protein monomers that are arranged like a barrel in the plasma membrane. Each subunit typically consists of six potential transmembrane segments (S1, S2, S3, S4, S5, and S6). The center of the barrel forms a pore lined by α -helices or β -strands. The side chains of the amino acid residues comprising the α -helices or β -strands establish the charge (cation or anion) selectivity of the channel. The degree of selectivity, or what specific ions are allowed to pass through the channel, depends on the diameter of the narrowest part of the pore. There

are two basic types of ion channels, ion transporters and gated ion channels. Ion transporters utilize the energy obtained from ATP hydrolysis to actively transport an ion against the ion's concentration gradient. Gated ion channels allow passive flow of an ion down the ion's electrochemical gradient under restricted conditions. Together, these types of ion channels generate, maintain, and utilize an electrochemical gradient that is used in 1) electrical impulse conduction down the axon of a nerve cell, 2) transport of molecules into cells against concentration gradients, 3) initiation of muscle contraction, and 4) endocrine cell secretion.

Transmembrane ATPases are divided into three families. The phosphorylated (P) class ion transporters, including Na⁺-K⁺ ATPase, Ca²⁺ ATPase, H⁺ ATPase, and Cu⁺⁺ ATPase, are activated by a phosphorylation event. P-class ion transporters are responsible for maintaining resting potential distributions such that cytosolic concentrations of Na⁺ and Ca²⁺ are low and cytosolic concentration of K⁺ is high. The vacuolar (V) class of ion transporters include H⁺ pumps on intracellular organelles, such as lysosomes and Golgi. V-class ion transporters are responsible for generating the low pH within the lumen of these organelles that is required for function. The coupling factor (F) class consists of H⁺ pumps in the mitochondria. F-class ion transporters utilize a proton gradient to generate ATP from ADP and inorganic phosphate (P_i).

Cu⁺⁺ ATPases export copper from cells (PROSITE PDOC00139 E1-E2 ATPases phosphorylation site). Mutations in one Cu⁺⁺ ATPase cause Wilson disease, in which toxic amounts of copper accumulate in a number of organs, particularly the liver and brain (Tanzi, R.E. et al. (1993) Nat. Genet. 5:344-350). Mutations in another Cu⁺⁺ ATPase cause Menkes disease and occipital horn syndrome. Menkes disease mutations block export of copper from the gastrointestinal tract, leading to skeletal abnormalities, severe mental retardation, neurologic degeneration, and mortality in early childhood (Harrison, M.D. and C.T. Dameron (1999) J. Biochem. Mol. Toxicol. 13:93-106). Occipital horn syndrome mutations cause connective tissue defects (Harrison, *supra*; Levinson, B. et al. (1996) Hum. Mol. Genet. 5:1737-1742).

The coupling factor (F) class of ion transporters consists of H⁺ pumps in mitochondria, chloroplasts, and bacteria. For example, the F₀F₁ ATPase utilizes a proton gradient across the inner mitochondrial membrane to generate ATP from ADP and inorganic phosphate (P_i). The F₀F₁ ATPase is composed of the F₀ complex, which is the transmembrane channel through which protons flow, and the F₁ complex, where ATP synthesis activity resides. F₀ has three subunits, A (also known as protein 6), B, and C (Lodish, H. et al. (1995) Molecular Cell Biology, Scientific American Books, New York NY, pp. 752-756; PROSITE PDOC00420 ATP synthase a subunit signature).

Voltage-gated Ca²⁺ channels are involved in presynaptic neurotransmitter release, and heart and skeletal muscle contraction. The voltage-gated Ca²⁺ channels from skeletal muscle (L-type) and brain (N-type) have been purified and, though their functions differ dramatically, they have similar subunit compositions. The channels are composed of three subunits. The α₁ subunit forms the

membrane pore and voltage sensor, while the $\alpha_2\delta$ and β subunits modulate the voltage-dependence, gating properties, and the current amplitude of the channel. These subunits are encoded by at least six α_1 , one $\alpha_2\delta$, and four β genes. A fourth subunit, γ , has been identified in skeletal muscle (Walker, D. et al. (1998) J. Biol. Chem. 273:2361-2367; and Jay, S.D. et al. (1990) Science 248:490-492). The

5 human β_4 subunit is homologous to the mouse epilepsy gene lethargic, and is a candidate for involvement in neurological disorders including ataxia and absence epilepsy (Escayg, A. et al. (1998) Genomics 50:14-22).

Ligand-gated channels open their pores when an extracellular or intracellular mediator binds to the channel. Neurotransmitter-gated channels are channels that open when a neurotransmitter

10 binds to their extracellular domain. These channels exist in the postsynaptic membrane of nerve or muscle cells. There are two types of neurotransmitter-gated channels. Sodium channels open in response to excitatory neurotransmitters, such as acetylcholine, glutamate, and serotonin. This opening causes an influx of Na^+ and produces the initial localized depolarization that activates the voltage-gated channels and starts the action potential. Chloride channels open in response to

15 inhibitory neurotransmitters, such as γ -aminobutyric acid (GABA) and glycine, leading to hyperpolarization of the membrane and the subsequent generation of an action potential.

Ion channels are expressed in a number of tissues where they are implicated in a variety of processes. CNG channels, while abundantly expressed in photoreceptor and olfactory sensory cells, are also found in kidney, lung, pineal, retinal ganglion cells, testis, aorta, and brain. Calcium-activated

20 K^+ channels may be responsible for the vasodilatory effects of bradykinin in the kidney and for shunting excess K^+ from brain capillary endothelial cells into the blood. They are also implicated in repolarizing granulocytes after agonist-stimulated depolarization (Ishi, T.M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11651-11656). Another transmembrane protein, the leukotriene B4 receptor (BLT) appears to be involved in inflammation responses and host cell defense against infection. BLT also

25 functions as an HIV coreceptor (Izumi, T. et al. (1997) Nature 387:620-624; Martin, V. et al. (1999) J. Biol. Chem. 274:8597-8603).

Ion channels have been the target for many drug therapies. Neurotransmitter-gated channels have been targeted in therapies for treatment of insomnia, anxiety, depression, and schizophrenia. Voltage-gated channels have been targeted in therapies for arrhythmia, ischemic stroke, head trauma,

30 and neurodegenerative disease (Taylor, C.P. and L.S. Narasimhan (1997) Adv. Pharmacol. 39:47-98).

K^+ channels are located in all cell types, and may be regulated by voltage, ATP concentration, or second messengers such as Ca^{++} and cAMP. In non-excitabile tissue, K^+ channels are involved in protein synthesis, control of endocrine secretions, and the maintenance of osmotic equilibrium across membranes. In neurons and other excitable cells, in addition to regulating action

35 potentials and repolarizing membranes, K^+ channels are responsible for setting resting membrane potential. The cytosol contains non-diffusible anions and, to balance this net negative charge, the cell

contains a Na^+ - K^+ pump and ion channels that provide the redistribution of Na^+ , K^+ , and Cl^- . The pump actively transports Na^+ out of the cell and K^+ into the cell in a 3:2 ratio. Ion channels in the plasma membrane allow K^+ and Cl^- to flow by passive diffusion. Because of the high negative charge within the cytosol, Cl^- flows out of the cell. The flow of K^+ is balanced by an electromotive force
 5 pulling K^+ into the cell, and a K^+ concentration gradient pushing K^+ out of the cell. Thus, the resting membrane potential is primarily regulated by K^+ flow (Salkoff, L. and T. Jegla (1995) *Neuron* 15:489-492). Information on NY-REN-45, a K^+ channel integral membrane protein, can be found in Scanlan, M.J. et al. (1998; *Int. J. Cancer* 76:652-658). The emopamil-binding protein (EBP) shares structural features with both pro- and eukaryotic drug transport proteins (Hanner, M. et al. (1995) *J.*
 10 *Biol. Chem.* 270:7551-7557). The Na^+ channel, transmembrane protein myelin protein zero (MPZ) may be responsible for some sporadic cases of Dejerine-Scottas disease (hereditary motor and sensory neuropathy type III) (Hayasaka, K. et al. (1993) *Nat. Genet.* 5:266-268).

K^+ pore-forming subunits generally have six transmembrane-spanning domains with a short region between the fifth and sixth transmembrane regions that senses membrane potential; and the
 15 amino and carboxy termini are located intracellularly. In mammalian heart, the duration of ventricular action potential is controlled by a K^+ current. Thus, the K^+ channel is central to the control of heart rate and rhythm. K^+ channel dysfunctions are associated with a number of renal diseases including hypertension, hypokalemia, and the associated Bartter's syndrome and Getelman's syndrome, as well as neurological disorders including epilepsy. K^+ channels have been implicated in
 20 Alzheimer's disease by observations that a significant component of senile plaques, beta amyloid or A beta, also blocks voltage-gated potassium channels in hippocampal neurons (Antes, L.M. et al. (1998) *Seminars Nephrol.* 18:31-45; Stoffel, M. and L.Y. Jan (1998) *Nat. Genet.* 18:6-8; Madeja, M. et al. (1997) *Eur. J. Neurosci.* 9:390-395; Good, T.A. et al. (1996) *Biophys. J.* 70:296-304).

Gated ion channels control ion flow by regulating the opening and closing of pores. These
 25 channels are categorized according to the manner of regulating the gating function. Mechanically-gated channels open pores in response to mechanical stress, voltage-gated channels open pores in response to changes in membrane potential, and ligand-gated channels open pores in the presence of a specific ion, nucleotide, or neurotransmitter.

Voltage-gated Na^+ channels are responsible for electrical excitability of neurons, skeletal
 30 muscle, heart, and neuroendocrine tissues. For example, the sequential opening and closing of voltage-gated Na^+ channels results in the propagation of action potentials down neuronal axons. Na^+ channels isolated from rat brain tissue are heterotrimeric complexes composed of a 260 kDa pore forming α subunit that associates with two smaller auxiliary subunits, $\beta 1$ and $\beta 2$. The $\beta 2$ subunit is an integral membrane glycoprotein that contains an extracellular Ig domain, and its association with α
 35 and $\beta 1$ subunits correlates with increased function of the channel, a change in the channel's gating properties, as well as an increase in whole cell capacitance (Isom, L.L. et al. (1995) *Cell* 83:433-442).

Integral Membrane Proteins

The majority of known integral membrane proteins are transmembrane proteins (TM) which are characterized by an extracellular, a transmembrane, and an intracellular domain. TM domains are typically comprised of 15 to 25 hydrophobic amino acids which are predicted to adopt an α -helical conformation. TM proteins are classified as bitopic (Types I and II) and polytopic (Types III and IV) (Singer, S.J. (1990) *Annu. Rev. Cell Biol.* 6:247-96). Bitopic proteins span the membrane once while polytopic proteins contain multiple membrane-spanning segments. TM proteins that act as cell-surface receptor proteins involved in signal transduction include growth and differentiation factor receptors, and receptor-interacting proteins such as Drosophila pecanex and frizzled proteins, LIV-1 protein, NF2 protein, and GNS1/SUR4 eukaryotic integral membrane proteins. TM proteins also act as transporters of ions or metabolites, such as gap junction channels (connexins) and ion channels, and as cell anchoring proteins, such as lectins, integrins, and fibronectins. TM proteins act as vesicle organelle-forming molecules, such as calveolins, or as cell recognition molecules, such as cluster of differentiation (CD) antigens, glycoproteins, and mucins. Information on connexin can be found in Kanter, H.L. et al. (1994; *J. Mol. Cell. Cardiol.* 26:861-868).

Many membrane proteins (MPs) contain amino acid sequence motifs that target these proteins to specific subcellular sites. Examples of these motifs include PDZ domains, KDEL, RGD, NGR, and GSL sequence motifs, von Willebrand factor A (vWFA) domains, and EGF-like domains. RGD, NGR, and GSL motif-containing peptides have been used as drug delivery agents in cancer treatments which target tumor vasculature (Arap, W. et al. (1998) *Science*, 279:377-380.) Furthermore, MPs may also contain amino acid sequence motifs, such as the carbohydrate recognition domain (CRD), also known as the C-type lectin domain, that mediate interactions with extracellular or intracellular molecules.

G-protein coupled receptors (GPCR) comprise a superfamily of integral membrane proteins which transduce extracellular signals. GPCRs include receptors for biogenic amines, lipid mediators of inflammation, peptide hormones, and sensory signal mediators. The structure of these highly-conserved receptors consists of seven hydrophobic transmembrane regions, an extracellular N-terminus, and a cytoplasmic C-terminus. Three extracellular loops alternate with three intracellular loops to link the seven transmembrane regions. The most conserved parts of these proteins are the transmembrane regions and the first two cytoplasmic loops. Cysteine disulfide bridges connect the second and third extracellular loops. A conserved, acidic-Arg-aromatic residue triplet present in the second cytoplasmic loop may interact with G proteins. A GPCR consensus pattern is characteristic of most proteins belonging to this superfamily (ExpASY PROSITE document PS00237; and Watson, S. and S. Arkinstall (1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego CA, pp 2-6). Mutations and changes in transcriptional activation of GPCR-encoding genes have been

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associated with neurological disorders such as schizophrenia, Parkinson's disease, Alzheimer's disease, drug addiction, and feeding disorders.

Cytochromes are electron-transferring proteins that contain a heme prosthetic group, a porphyrin ring containing a tightly bound iron atom. Cytochromes act as oxidoreductases in such
 5 diverse cellular processes as respiration, photosynthesis, fatty acid metabolism, and neurotransmitter biosynthesis. The heme iron atom serves as the actual electron carrier by changing from the ferric to the ferrous oxidation state when accepting an electron. Cytochromes accept electrons from one substrate such as NADH or ascorbate and donate them to other electron carriers such as other cytochromes, ubiquinone, or semidehydroascorbic acid (Lodish, H. et al. (1995) Molecular Cell
 10 Biology, Scientific American Books, New York NY, pp. 759-770, 786-797; Sperling, P. et al. (1995) Eur. J. Biochem. 232:798-805; and Online Mendelian Inheritance in Man (OMIM) *600019 Cytochrome b561, CYB561).

Cytochrome b5 is an electron donor in membrane-linked redox enzyme systems involved in lipid and drug metabolism. Cytochrome b5 has been found in Golgi, plasma, outer mitochondrial,
 15 endoplasmic reticulum (ER), and microbody membranes. Conserved amino acids in cytochrome b5 include eight invariant amino acids at W34, H51, P52, G53, G54, G63, F70, and H74, and fifteen conserved amino acids at L24, I35, S36, V41, Y42, N43, T45, W47, A48, L58, D65, T67, L85, T87, and G88 (numbering based on the sunflower cytochrome b5/delta-6 desaturase fusion protein; GI 1040729, Sperling, supra). The invariant residues H51PGG are involved in heme-binding.
 20 Cytochrome b5-like domains have also been found linked to other enzymes. For example, cytochrome b5-like domains are part of delta-9 fatty acid desaturases in yeast and Histoplasma capsulatum, nitrate reductase, sulfite reductase, flavocytochrome b2, Arabidopsis thaliana acyl lipid desaturase, and Borago officinalis (borage) and Helianthus annuus (sunflower) delta-6 desaturases (Sperling, supra; Sayanova, O. et al (1997) Proc. Natl. Acad. Sci. USA 94:4211-4216; and Mitchell, A.G. and C.E. Martin (1997) J. Biol. Chem. 272:28281-28288).
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Signal peptides are found on proteins that are targeted to the endoplasmic reticulum (ER). Signal peptides consist of stretches of amino acids enriched in hydrophobic residues. Signal peptides are usually found at the extreme N-terminus of the protein and are recognized by a cytosolic signal-recognition peptide (SRP). The SRP binds to the signal peptide and to an SRP receptor, an integral
 30 membrane protein in the ER. Once bound to the SRP receptor, the newly formed protein containing the signal peptide is translocated across the ER membrane. Proteins containing signal peptides may end up inserted into the lipid bilayer, or they may end up in the lumen of an organelle or secreted from the cell.

35 Disease Correlation

The etiology of numerous human diseases and disorders can be attributed to defects in the

transport of molecules across membranes. Defects in the trafficking of membrane-bound transporters and ion channels are associated with several disorders, e.g. cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, von Gierke disease, and certain forms of diabetes mellitus. Single-gene defect diseases resulting in an inability to transport small molecules across
 5 membranes include, e.g., cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease (van't Hoff, W.G. (1996) *Exp. Nephrol.* 4:253-262; Talente, G.M. et al. (1994) *Ann. Intern. Med.* 120:218-226; and Chillon, M. et al. (1995) *New Engl. J. Med.* 332:1475-1480).

Cystinuria is an inherited disease that results from the inability to transport cystine, the disulfide-linked dimer of cysteine, from the urine into the blood. Accumulation of cystine in the
 10 urine leads to the formation of cystine stones in the kidneys.

Transthyretin (TTR), present in human plasma, binds to and transports the thyroid hormone thyroxine. Mutations in TTR result in the conversion of TTR to amyloid, an insoluble fibrillar structure. The resulting amyloid plaques have been shown to be the causative agent in the development of familial amyloid polyneuropathy and senile systemic amyloidosis (Mirov, G.J. et al.
 15 (1996) *Proc. Natl. Acad. Sci. USA* 93:15051-15056).

Stomatin, a 31-kDa erythrocyte integral membrane protein has been linked to the hereditary anemia stomatocytosis. This anemia is characterized by red blood cells that lack stomatin and leak Na⁺ and K⁺. Thus, stomatin is presumed to play a role in the regulation of ion transport. Red blood cell ion transport defects are also linked to other disorders such as hypertension (Stewart, G.W.
 20 (1997) *Int. J. Biochem. Cell Biol.* 29:271-274).

The discovery of new human transport proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of transport, metabolic, neurological, cardiovascular, reproductive, and
 25 immune disorders, and cell proliferative disorders including cancer.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, human transport proteins, referred to collectively as "TPPT" and individually as "TPPT-1," "TPPT-2," "TPPT-3," "TPPT-4," "TPPT-5,"
 30 "TPPT-6," "TPPT-7," "TPPT-8," "TPPT-9," "TPPT-10," "TPPT-11," "TPPT-12," "TPPT-13," "TPPT-14," "TPPT-15," "TPPT-16," "TPPT-17," "TPPT-18," "TPPT-19," "TPPT-20," "TPPT-21," "TPPT-22," "TPPT-23," "TPPT-24," "TPPT-25," "TPPT-26," "TPPT-27," "TPPT-28," "TPPT-29," "TPPT-30," "TPPT-31," "TPPT-32," "TPPT-33," "TPPT-34," "TPPT-35," "TPPT-36," "TPPT-37," "TPPT-38," "TPPT-39," "TPPT-40," "TPPT-41," "TPPT-42," and "TPPT-43." In one aspect, the
 35 invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-

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- 43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-43.

- The invention further provides an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-43. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:44-86.

- Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

- The invention also provides a method for producing a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a

polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence
 5 selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43.

The invention further provides an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:44-86, b) a naturally occurring polynucleotide sequence having at least 70%
 10 sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:44-86, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a
 15 sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:44-86, b) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:44-86, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary
 20 to b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said
 25 hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group
 30 consisting of SEQ ID NO:44-86, b) a naturally occurring polynucleotide sequence having at least 70% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:44-86, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting
 35 the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a pharmaceutical composition comprising an effective amount of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and a pharmaceutically acceptable excipient. In one embodiment, the pharmaceutical composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional TPPT, comprising administering to a patient in need of such treatment the pharmaceutical composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional TPPT, comprising administering to a patient in need of such treatment the pharmaceutical composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional TPPT, comprising administering to a patient in

need of such treatment the pharmaceutical composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-43. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:44-86, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

BRIEF DESCRIPTION OF THE TABLES

Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding TPPT.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods, algorithms, and searchable databases used for analysis of TPPT.

Table 3 shows selected fragments of each nucleic acid sequence; the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis; diseases, disorders, or conditions associated with these tissues; and the vector into which each cDNA was cloned.

5 Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding TPPT were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

10

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing
15 particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a
20 reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be
25 used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

30 DEFINITIONS

"TPPT" refers to the amino acid sequences of substantially purified TPPT obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of
35 TPPT. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TPPT either by directly interacting with

TPPT or by acting on components of the biological pathway in which TPPT participates.

An "allelic variant" is an alternative form of the gene encoding TPPT. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or
5 many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding TPPT include those sequences with deletions,
10 insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as TPPT or a polypeptide with at least one functional characteristic of TPPT. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding TPPT, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding
15 TPPT. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent TPPT. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of TPPT is retained. For example,
20 negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

25 The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

30 "Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of TPPT. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small
35 molecules, or any other compound or composition which modulates the activity of TPPT either by directly interacting with TPPT or by acting on components of the biological pathway in which TPPT

participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind TPPT polypeptides can be prepared using intact polypeptides or using fragments
5 containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

10 The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen
15 used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified
20 sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or
25 translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic TPPT, or of any oligopeptide thereof,
30 to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

35 A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or

amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding TPPT or fragments of TPPT may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be
 5 deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (PE Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from
 10 one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least
 15 interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
20	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
25	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
30	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
35	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

40 Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide sequence can include, for example, replacement of
 5 hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

10 A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

A "fragment" is a unique portion of TPPT or the polynucleotide encoding TPPT which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a
 15 fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected
 20 from the first 250 or 500 amino acids (or first 25% or 50% of a polypeptide) as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:44-86 comprises a region of unique polynucleotide sequence that
 25 specifically identifies SEQ ID NO:44-86, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:44-86 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:44-86 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:44-86 and the region of SEQ ID NO:44-86 to which the fragment corresponds are routinely
 30 determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-43 is encoded by a fragment of SEQ ID NO:44-86. A fragment of SEQ ID NO:1-43 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-43. For example, a fragment of SEQ ID NO:1-43 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-43. The precise length of
 35 a fragment of SEQ ID NO:1-43 and the region of SEQ ID NO:1-43 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended

purpose for the fragment.

A "full-length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full-length" polynucleotide sequence encodes a "full-length" polypeptide sequence.

5 "Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps
10 in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of
15 molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent
20 similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at
25 <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The
30 "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

35 *Reward for match: 1*

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

5 *Filter: on*

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous
10 nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes
15 in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some
20 alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e
25 sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

30 Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12 (Apr-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

35 *Open Gap: 11 and Extension Gap: 1 penalties*

Gap x drop-off: 50

WO 00/78953

PCT/US00/16668

*Expect: 10**Word Size: 3**Filter: on*

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking
 5 reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency
 10 conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one
 15 nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.
 20 "Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of TPPT which is
 25 capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of TPPT which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides,
 30 polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of TPPT. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other
 35 biological, functional, or immunological properties of TPPT.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide,

polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

"Post-translational modification" of an TPPT may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of TPPT.

"Probe" refers to nucleic acid sequences encoding TPPT, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule.

Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.

"Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs

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can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is

expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription,
5 translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

10 An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic
15 acids encoding TPPT, or fragments thereof, or TPPT itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or
20 synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

25 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides
30 by different amino acid residues or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

35 A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants, and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide

polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

10 THE INVENTION

The invention is based on the discovery of new human transport proteins (TPPT), the polynucleotides encoding TPPT, and the use of these compositions for the diagnosis, treatment, or prevention of transport, metabolic, neurological, cardiovascular, reproductive, and immune disorders, and cell proliferative disorders including cancer.

15 Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding TPPT. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each TPPT were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA
20 libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. In some cases, GenBank sequence identifiers are also shown in column 5. The Incyte clones and GenBank cDNA sequences, where indicated, in column 5 were used to assemble the consensus nucleotide sequence of each TPPT and are useful as fragments in hybridization technologies.

25 The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows homologous sequences as identified by BLAST analysis; and column 7 shows analytical
30 methods and in some cases, searchable databases to which the analytical methods were applied. The methods of column 7 were used to characterize each polypeptide through sequence homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding TPPT. The first column of Table 3 lists the nucleotide
35 SEQ ID NOs. Column 2 lists fragments of the nucleotide sequences of column 1. These fragments are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:44-86

and to distinguish between SEQ ID NO:44-86 and related polynucleotide sequences. The polypeptides encoded by these fragments are useful, for example, as immunogenic peptides. Column 3 lists tissue categories which express TPPT as a fraction of total tissues expressing TPPT. Column 4 lists diseases, disorders, or conditions associated with those tissues expressing TPPT as a fraction of total tissues expressing TPPT. Column 5 lists the vectors used to subclone each cDNA library.

Of particular interest is the expression of SEQ ID NO:50 exclusively in cardiovascular tissue, the expression of SEQ ID NO:56 in nervous and gastrointestinal tissues, the expression of SEQ ID NO:57 in gastrointestinal tissues, and the expression of SEQ ID NO:66 in nervous system tissues. Of particular note is the tissue-specific expression of SEQ ID NO:75. Over 71% of the cDNA libraries expressing SEQ ID NO:75 are derived from lung tissue.

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding TPPT were isolated. Column 1 references the nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

SEQ ID NO:44 maps to chromosome 7 within the interval from 38.80 to 42.10 centiMorgans. SEQ ID NO:48 maps to chromosome X within the interval from 107.90 to 122.80 centiMorgans. SEQ ID NO:60 maps to chromosome 2 within the interval from 157.0 to 167.0 centiMorgans. SEQ ID NO:65 maps to chromosome 2 within the interval from 17.4 to 40.7 centiMorgans and to chromosome 5 within the interval from 61.1 to 69.6 centiMorgans. The interval on chromosome 5 from 61.1 to 69.6 centiMorgans also contains genes associated with Cockayne syndrome. SEQ ID NO:69 maps to chromosome 3 within the interval from 157.40 to 162.00 centiMorgans. SEQ ID NO:70 maps to chromosome 3 within the interval from 176.40 to 179.80 centiMorgans. SEQ ID NO:71 maps to chromosome 18 within the interval from the p-terminus to 52.30 centiMorgans. SEQ ID NO:73 maps to chromosome 17 within the interval from 75.70 to 84.20 centiMorgans, and to chromosome 2 within the interval from 204.70 to 209.30 centiMorgans. SEQ ID NO:76 maps to chromosome 20 within the interval from 79.00 to 94.40 centiMorgans. SEQ ID NO:80 maps to chromosome 18 within the interval from 1.60 to 6.20 centiMorgans, and to chromosome 11 within the interval from 117.90 to 126.00 centiMorgans. SEQ ID NO:83 maps to chromosome 17 within the interval from 67.60 to 69.30 centiMorgans, and from 83.8 centiMorgans to the q-terminus, and to chromosome 7 within the interval from 105.20 to 114.50 centiMorgans.

The invention also encompasses TPPT variants. A preferred TPPT variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the TPPT amino acid sequence, and which contains at least one functional or structural characteristic of TPPT.

The invention also encompasses polynucleotides which encode TPPT. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected

from the group consisting of SEQ ID NO:44-86, which encodes TPPT. The polynucleotide sequences of SEQ ID NO:44-86, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

5 The invention also encompasses a variant of a polynucleotide sequence encoding TPPT. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding TPPT. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:44-
10 86 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:44-86. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of TPPT.

 It will be appreciated by those skilled in the art that as a result of the degeneracy of the
15 genetic code, a multitude of polynucleotide sequences encoding TPPT, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the
20 polynucleotide sequence of naturally occurring TPPT, and all such variations are to be considered as being specifically disclosed.

 Although nucleotide sequences which encode TPPT and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring TPPT under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding TPPT or
25 its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding TPPT and its derivatives without altering the encoded amino acid sequences
30 include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

 The invention also encompasses production of DNA sequences which encode TPPT and TPPT derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems
35 using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding TPPT or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:44-86 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (PE Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (PE Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (PE Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding TPPT may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) *PCR Methods Applic.* 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) *Nucleic Acids Res.* 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) *PCR Methods Applic.* 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) *Nucleic Acids Res.* 19:3055-3060.) Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo

Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, PE Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode TPPT may be cloned in recombinant DNA molecules that direct expression of TPPT, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express TPPT.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter TPPT-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or

improve the biological properties of TPPT, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding TPPT may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.) Alternatively, TPPT itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (PE Biosystems). Additionally, the amino acid sequence of TPPT, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active TPPT, the nucleotide sequences encoding TPPT or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding TPPT. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding TPPT. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding TPPT and its initiation codon and upstream regulatory sequences are inserted into

the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both
 5 natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding TPPT and appropriate transcriptional and translational control
 10 elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences
 15 encoding TPPT. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or
 20 animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945; Takamatsu, N. (1987) *EMBO J.* 6:307-311; Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984)
 25 *Science* 224:838-843; Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659; and Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences
 30 to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) *Cancer Gen. Ther.* 5(6):350-356; Yu, M. et al., (1993) *Proc. Natl. Acad. Sci. USA* 90(13):6340-6344; Buller, R.M. et al. (1985) *Nature* 317(6040):813-815; McGregor, D.P. et al. (1994) *Mol. Immunol.* 31(3):219-226; and Verma, I.M. and N. Somia (1997) *Nature* 389:239-242.) The invention is not limited by the host cell employed.

35 In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding TPPT. For example, routine cloning,

subcloning, and propagation of polynucleotide sequences encoding TPPT can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding TPPT into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of TPPT are needed, e.g. for the production of antibodies, vectors which direct high level expression of TPPT may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of TPPT. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, supra; and Scorer, supra.)

Plant systems may also be used for expression of TPPT. Transcription of sequences encoding TPPT may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, supra; Broglie, supra; and Winter, supra.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding TPPT may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses TPPT in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet.

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15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of TPPT in cell lines is preferred. For example, sequences encoding TPPT can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk⁻* and *apr⁻* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding TPPT is inserted within a marker gene sequence, transformed cells containing sequences encoding TPPT can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding TPPT under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding TPPT and that express TPPT may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or

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chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of TPPT using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and
 5 fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on TPPT is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and
 10 Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding TPPT
 15 include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding TPPT, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety
 20 of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding TPPT may be cultured under
 25 conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode TPPT may be designed to contain signal sequences which direct secretion of TPPT through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity.
 35 Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the

American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding TPPT may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric TPPT protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of TPPT activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the TPPT encoding sequence and the heterologous protein sequence, so that TPPT may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled TPPT may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

TPPT of the present invention or fragments thereof may be used to screen for compounds that specifically bind to TPPT. At least one and up to a plurality of test compounds may be screened for specific binding to TPPT. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of TPPT, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which TPPT binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express TPPT, either as a secreted

protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing TPPT or cell membrane fractions which contain TPPT are then contacted with a test compound and binding, stimulation, or inhibition of activity of either TPPT or the compound is analyzed.

5 An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with TPPT, either in solution or affixed to a solid support, and detecting the binding of TPPT to the compound.

Alternatively, the assay may detect or measure binding of a test compound in the presence of a
10 labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

TPPT of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of TPPT. Such compounds may include agonists, antagonists, or partial or
15 inverse agonists. In one embodiment, an assay is performed under conditions permissive for TPPT activity, wherein TPPT is combined with at least one test compound, and the activity of TPPT in the presence of a test compound is compared with the activity of TPPT in the absence of the test compound. A change in the activity of TPPT in the presence of the test compound is indicative of a compound that modulates the activity of TPPT. Alternatively, a test compound is combined with an
20 in vitro or cell-free system comprising TPPT under conditions suitable for TPPT activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of TPPT may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding TPPT or their mammalian homologs may
25 be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of
30 interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids
35 Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred

to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding TPPT may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding TPPT can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding TPPT is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress TPPT, e.g., by secreting TPPT in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of TPPT and human transport proteins. In addition, the expression of TPPT is closely associated with neurological, cardiovascular, reproductive, gastrointestinal, and hematopoietic/immune tissues, and inflammation, cell proliferation, and cancer. Therefore, TPPT appears to play a role in transport, metabolic, neurological, cardiovascular, reproductive, and immune disorders, and cell proliferative disorders including cancer. In the treatment of disorders associated with increased TPPT expression or activity, it is desirable to decrease the expression or activity of TPPT. In the treatment of disorders associated with decreased TPPT expression or activity, it is desirable to increase the expression or activity of TPPT.

Therefore, in one embodiment, TPPT or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TPPT. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer; cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline

- myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis; neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia; and other
- 5 disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn
- 10 syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease; a metabolic disorder such as Addison's disease, cerebrotendinous xanthomatosis, congenital adrenal hyperplasia, coumarin resistance, cystic fibrosis, diabetes, fatty hepatocirrhosis, fructose-1,6-diphosphatase deficiency, galactosemia, goiter, glucagonoma, glycogen storage diseases, hereditary fructose intolerance, hyperadrenalism, hypoadrenalism, hyperparathyroidism,
- 15 hypoparathyroidism, hypercholesterolemia, hyperthyroidism, hypoglycemia, hypothyroidism, hyperlipidemia, hyperlipemia, lipid myopathies, lipodystrophies, lysosomal storage diseases, mannosidosis, neuraminidase deficiency, obesity, pentosuria phenylketonuria, and pseudovitamin D-deficiency rickets; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's
- 20 disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and
- 25 Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders,
- 30 peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial
- 35 frontotemporal dementia; a cardiovascular disorder such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins,

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- thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve,
- 5 mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary
- 10 hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis,
- 15 pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; a
- 20 reproductive disorder such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; a disruption of spermatogenesis, abnormal sperm
- 25 physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis,
- 30 autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia,
- 35 irritable bowel syndrome, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis,

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pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, 5 fungal, parasitic, protozoal, and helminthic infections, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, 10 myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing TPPT or a fragment or derivative 15 thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TPPT including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified TPPT in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TPPT including, but not 20 limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of TPPT may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TPPT including, but not limited to, those listed above.

In a further embodiment, an antagonist of TPPT may be administered to a subject to treat or 25 prevent a disorder associated with increased expression or activity of TPPT. Examples of such disorders include, but are not limited to, those transport, metabolic, neurological, cardiovascular, reproductive, and immune disorders, and cell proliferative disorders including cancer described above. In one aspect, an antibody which specifically binds TPPT may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to 30 cells or tissues which express TPPT.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding TPPT may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TPPT including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary 35 sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made

by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

5 An antagonist of TPPT may be produced using methods which are generally known in the art. In particular, purified TPPT may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind TPPT. Antibodies to TPPT may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and
10 fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with TPPT or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to
15 increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to TPPT
20 have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of TPPT amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

25 Monoclonal antibodies to TPPT may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and
30 Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda,
35 S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce TPPT-specific single

chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte
 5 population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for TPPT may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin
 10 digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired
 15 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between TPPT and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering TPPT epitopes is generally used, but a competitive binding assay may
 20 also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for TPPT. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of TPPT-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions.
 25 The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple TPPT epitopes, represents the average affinity, or avidity, of the antibodies for TPPT. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular TPPT epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the
 30 TPPT-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of TPPT, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons,
 35 New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to

determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of TPPT-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines
 5 for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al., supra.)

In another embodiment of the invention, the polynucleotides encoding TPPT, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA,
 10 RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding TPPT. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding TPPT. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense
 15 sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral
 20 vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.*
 25 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding TPPT may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined
 30 immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal,
 35 R.G. (1995) *Science* 270:404-410; Verma, I.M. and Somia, N. (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated

cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in TPPT expression or regulation causes disease, the expression of TPPT from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in TPPT are treated by constructing mammalian expression vectors encoding TPPT and introducing these vectors by mechanical means into TPPT-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of TPPT include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). TPPT may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and H.M. Blau, supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding TPPT from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to TPPT expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding TPPT under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. USA 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and A.D. Miller (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding TPPT to cells which have one or more genetic abnormalities with respect to the expression of TPPT. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544; and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding TPPT to target cells which have one or more genetic abnormalities with respect to the expression of TPPT. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing TPPT to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has

been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) *Exp. Eye Res.* 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) *J. Virol.* 73:519-532 and Xu, H. et al. (1994) *Dev. Biol.* 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding TPPT to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) *Curr. Opin. Biotech.* 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for TPPT into the alphavirus genome in place of the capsid-coding region results in the production of a large number of TPPT-coding RNAs and the synthesis of high levels of TPPT in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) *Virology* 228:74-83). The wide host range of alphaviruses will allow the introduction of TPPT into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have

been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

5 Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding TPPT.

10 Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of
15 candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis.
20 Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding TPPT. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

25 RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine,
30 and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding TPPT. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not
35 limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular

chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased TPPT expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding TPPT may be therapeutically useful, and in the treatment of disorders associated with decreased TPPT expression or activity, a compound which specifically promotes expression of the polynucleotide encoding TPPT may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding TPPT is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding TPPT are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding TPPT. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved

using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and
5 monkeys.

An additional embodiment of the invention relates to the administration of a pharmaceutical composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest
10 edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such pharmaceutical compositions may consist of TPPT, antibodies to TPPT, and mimetics, agonists, antagonists, or inhibitors of TPPT.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial,
15 intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Pharmaceutical compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol
20 delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration
25 enhancers.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of pharmaceutical compositions may be prepared for direct intracellular
30 delivery of macromolecules comprising TPPT or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, TPPT or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system
35 (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell

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culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

5 A therapeutically effective dose refers to that amount of active ingredient, for example TPPT or fragments thereof, antibodies of TPPT, and agonists, antagonists or inhibitors of TPPT, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose
10 lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with
15 little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

 The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the
20 severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

25 Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells,
30 conditions, locations, etc.

DIAGNOSTICS

 In another embodiment, antibodies which specifically bind TPPT may be used for the diagnosis of disorders characterized by expression of TPPT, or in assays to monitor patients being treated with TPPT or agonists, antagonists, or inhibitors of TPPT. Antibodies useful for diagnostic
35 purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for TPPT include methods which utilize the antibody and a label to detect TPPT in human body fluids

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or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring TPPT, including ELISAs, RIAs, and FACS, are known
5 in the art and provide a basis for diagnosing altered or abnormal levels of TPPT expression. Normal or standard values for TPPT expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibody to TPPT under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of TPPT expressed in subject,
10 control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding TPPT may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and
15 quantify gene expression in biopsied tissues in which expression of TPPT may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of TPPT, and to monitor regulation of TPPT levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding TPPT or closely related molecules may be used to
20 identify nucleic acid sequences which encode TPPT. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding TPPT, allelic variants, or related sequences.

25 Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the TPPT encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:44-86 or from genomic sequences including promoters, enhancers, and introns of the TPPT gene.

Means for producing specific hybridization probes for DNAs encoding TPPT include the
30 cloning of polynucleotide sequences encoding TPPT or TPPT derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels,
35 such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding TPPT may be used for the diagnosis of disorders

associated with expression of TPPT. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer; cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis; neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia; and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease; a metabolic disorder such as Addison's disease, cerebrotendinous xanthomatosis, congenital adrenal hyperplasia, coumarin resistance, cystic fibrosis, diabetes, fatty hepatocirrhosis, fructose-1,6-diphosphatase deficiency, galactosemia, goiter, glucagonoma, glycogen storage diseases, hereditary fructose intolerance, hyperadrenalism, hypoadrenalism, hyperparathyroidism, hypoparathyroidism, hypercholesterolemia, hyperthyroidism, hypoglycemia, hypothyroidism, hyperlipidemia, hyperlipemia, lipid myopathies, lipodystrophies, lysosomal storage diseases, mannosidosis, neuraminidase deficiency, obesity, pentosuria phenylketonuria, and pseudovitamin D-deficiency rickets; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial

nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia,

5 catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a cardiovascular disorder such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon

10 angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus

15 erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease,

20 emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary

25 hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; a reproductive disorder such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, a disruption of the estrous cycle, a

30 disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and

35 gynecomastia; an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome,

allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding TPPT may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered TPPT expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding TPPT may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding TPPT may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding TPPT in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

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In order to provide a basis for the diagnosis of a disorder associated with expression of TPPT, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding TPPT, under conditions suitable for hybridization or amplification.

5 Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

10 Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

15 With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development
20 or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding TPPT may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced *in vitro*. Oligomers will preferably contain a fragment of a polynucleotide encoding TPPT, or a fragment of a polynucleotide complementary to the polynucleotide encoding
25 TPPT, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding TPPT may be used to detect single nucleotide polymorphisms (SNPs). SNPs are
30 substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding TPPT are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal
35 tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are

detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual
 5 overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

10 Methods which may also be used to quantify the expression of TPPT include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of
 15 interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large
 20 numbers of genes simultaneously as described in Seilhamer, J.J. et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 5,840,484, incorporated herein by reference. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and
 25 monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

30 In another embodiment, antibodies specific for TPPT, or TPPT or fragments thereof may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci.
 35 USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-

2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding TPPT may be used
 5 to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a
 10 chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop
 15 genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, e.g., Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic
 20 map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding TPPT on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as
 25 linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely
 30 localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

35 In another embodiment of the invention, TPPT, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug

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screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between TPPT and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with TPPT, or fragments thereof, and washed. Bound TPPT is then detected by methods well known in the art. Purified TPPT can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding TPPT specifically compete with a test compound for binding TPPT. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with TPPT.

In additional embodiments, the nucleotide sequences which encode TPPT may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications and publications, mentioned above and below, in particular U.S. Ser. No. 60/139,923, U.S. Ser. No. 60/148,177, U.S. Ser. No. 60/149,357, and U.S. Ser. No. 60/162,287, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated

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using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

- 5 In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic
- 10 oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g.,
- 15 PBLUESCRIPT plasmid (Stratagene), PSORT1 plasmid (Life Technologies), pcDNA2.1 plasmid (Invitrogen, Carlsbad CA), or pINCY plasmid (Incyte Genomics, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

- 20 Plasmids obtained as described in Example I were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96
- 25 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

- Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in
- 30 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

- Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows.
- 35 Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (PE Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ

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Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems). Electrophoretic
 5 separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (PE Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some
 10 of the cDNA sequences were selected for extension using the techniques disclosed in Example VI.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools,
 15 programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO
 20 software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments were generated using the default parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programing, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and PFAM to acquire
 30 annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying
 35 against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and Hidden Markov Model (HMM)-based protein family databases such

as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID
5 NO:44-86. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs
10 from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer
15 search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair
25 (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced
30 either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding TPPT occurred. Analysis involved the categorization of cDNA libraries by
35 organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous,

reproductive, and urologic. The disease/condition categories included cancer, inflammation, trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in

5 Table 3.

V. Chromosomal Mapping of TPPT Encoding Polynucleotides

The cDNA sequences which were used to assemble SEQ ID NO:44-49 and SEQ ID NO:54-86 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these
10 databases that matched SEQ ID NO:44-49 and SEQ ID NO:54-86 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 5). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a
15 mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

The genetic map locations of SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:65, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:76, SEQ ID NO:80, and SEQ ID NO:83 are described in The Invention as ranges, or intervals, of human
20 chromosomes. More than one map location is reported for SEQ ID NO:65, SEQ ID NO:73, SEQ ID NO:80, and SEQ ID NO:83, indicating that previously mapped sequences having similarity, but not complete identity, to SEQ ID NO:65, SEQ ID NO:73, SEQ ID NO:80, and SEQ ID NO:83 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of
25 measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Diseases associated with the public and Incyte sequences located within the
30 indicated intervals are also reported in the Invention section where applicable. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

VI. Extension of TPPT Encoding Polynucleotides

35 The full length nucleic acid sequences of SEQ ID NO:44-86 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this

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fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target
 5 sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR
 10 was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C,
 15 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN
 20 quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by
 25 electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For
 30 shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on
 35 antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems).

In like manner, the polynucleotide sequences of SEQ ID NO:44-86 are used to obtain 5' regulatory sequences using the procedure above, along with oligonucleotides designed for such extension, and an appropriate genomic library.

VII. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:44-86 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

VIII. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers.

Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g.,

- 5 Schena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31.)

- Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The
10 array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of
15 complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

- Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and
20 poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with
25 GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37 °C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85 °C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc.
30 (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μl 5X SSC/0.2% SDS.

Microarray Preparation

- 35 Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification

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uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

5 Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C
10 oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

15 Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60 °C followed by washes in 0.2% SDS and distilled water as before.

20 Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65 °C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly
25 larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60 °C. The arrays are washed for 10 min at 45 °C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45 °C in a second wash buffer (0.1X SSC), and dried.

Detection

30 Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-
35 scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

IX. Complementary Polynucleotides

Sequences complementary to the TPPT-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring TPPT. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of TPPT. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the TPPT-encoding transcript.

X. Expression of TPPT

Expression and purification of TPPT is achieved using bacterial or virus-based expression systems. For expression of TPPT in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express TPPT upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of TPPT in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding TPPT by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, TPPT is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from TPPT at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified TPPT obtained by these methods can be used directly in the assays shown in Examples XI and XV.

30 XI. Demonstration of TPPT Activity

TPPT transport activity is assayed by measuring uptake of labeled substrates into Xenopus laevis oocytes. Oocytes at stages V and VI are injected with TPPT mRNA (10 ng per oocyte) and incubated for 3 days at 18°C in OR2 medium (82.5mM NaCl, 2.5 mM KCl, 1mM CaCl₂, 1mM MgCl₂, 1mM Na₂HPO₄, 5 mM Hepes, 3.8 mM NaOH, 50µg/ml gentamycin, pH 7.8) to allow expression of TPPT. Oocytes are then transferred to standard uptake medium (100mM NaCl, 2 mM KCl, 1mM CaCl₂, 1mM MgCl₂, 10 mM Hepes/Tris pH 7.5). Uptake of various substrates (e.g., amino acids,

sugars, drugs, ions, and neurotransmitters) is initiated by adding labeled substrate (e.g. radiolabeled with ^3H , fluorescently labeled with rhodamine, etc.) to the oocytes. After incubating for 30 minutes, uptake is terminated by washing the oocytes three times in Na^+ -free medium, measuring the incorporated label, and comparing with controls. TPPT activity is proportional to the level of internalized labeled substrate.

XII. Functional Assays

TPPT function is assessed by expressing the sequences encoding TPPT at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT plasmid (Life Technologies) and pCR3.1 plasmid (Invitrogen), both of which contain the cytomegalovirus promoter. 5-10 μg of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μg of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of TPPT on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding TPPT and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding TPPT and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIII. Production of TPPT Specific Antibodies

TPPT substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

5 Alternatively, the TPPT amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

10 Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using FMOC chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide and anti-TPPT activity by, for example, binding the peptide or TPPT to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIV. Purification of Naturally Occurring TPPT Using Specific Antibodies

Naturally occurring or recombinant TPPT is substantially purified by immunoaffinity chromatography using antibodies specific for TPPT. An immunoaffinity column is constructed by covalently coupling anti-TPPT antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing TPPT are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TPPT (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/TPPT binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and TPPT is collected.

XV. Identification of Molecules Which Interact with TPPT

TPPT, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled TPPT, washed, and any wells with labeled TPPT complex are assayed. Data obtained using different concentrations of TPPT are used to calculate values for the number, affinity, and association of TPPT with the candidate molecules.

35 Alternatively, molecules interacting with TPPT are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989, *Nature* 340:245-246), or using commercially

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available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

TPPT may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent
5 No. 6,057,101).

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be
10 understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
13	56	1429651	SINTBST01	1429651F1 (SINTBST01), 1429651H1 (SINTBST01), 1501096F6 (SINTBST01), 1989621T6 (CORPNOT02), SXLA01343V1, SXLA01183V1, SXLA01559V1, SXLA00812V1
14	57	2069971	ISLTNOT01	2069606F6 (ISLTNOT01), 2069971H1 (ISLTNOT01), 2374634F6 (ISLTNOT01), 2383754F6 (ISLTNOT01), 4171186T6 (SINTNOT21), SXLA01128V1, SXLA01348V1, SXLA01219V1, SXLA00260V1, SXLA00074V1
15	58	2329339	COLNNOT11	658662H1 (BRAINOT03), 1544110R1 (PROSTUT04), 1657742F6 (URETTUT01), 1750523F6 (STOMTUT02), 2329339H1 (COLNNOT11), 2329339R6 (COLNNOT11), 3858671H1 (LNODNOT03), g1494061, g1891451
16	59	2540219	BONRTUT01	2540219H1 (BONRTUT01), 2540219T6 (BONRTUT01), 2554869F6 (THYMNOT03), g869197
17	60	2722462	LUNGTUT10	883601R1 (PANCNOT05), 1525902F6 (UCMCL5T01), 1525902X18C1 (UCMCL5T01), 1525902X11D1 (UCMCL5T01), 1527325T6 (UCMCL5T01), 1554770X311D1 (BLADTUT04), 2417265H1 (HNT3AZT01), 2444786F6 (THP1NOT03), 2722462H1 (LUNGTUT10), 4293114H1 (BRABDIR01), 5070268T6 (PANCNOT23), SANA01850F1, SAJA01078R1, SANA02081F1, SAJA01813F1
18	61	2739264	OVARNOT09	000573H1 (U937NOT01), 494409F1 (HNT2NOT01), 494409R1 (HNT2NOT01), 2506506F6 (CONUTUT01), 2681059H1 (SINIUCT01), 2744648F6 (BRSTTUT14), 2805590F6 (BLADTUT08), 3770643H1 (BRSTNOT25), 4204278H1 (BRAITUT29), SAEA02093F1
19	62	2758310	THP1AZS08	487309R7 (HNT2AGT01), 1361439F1 (LUNGNOT12), 2758310H1 (THP1AZS08), SCFA05584V1, SCFA05940V1, SCFA05166V1, SCFA05135V1
20	63	2762348	BRSTNOT12	632097R6 (KIDNNOT05), 632097T6 (KIDNNOT05), 2762348H1 (BRSTNOT12), SCCA02837V1, SCCA05356V1, SCCA01377V1, SCCA05963V1, SCCA05364V1, SCCA02307V1, SCCA04327V1, SCCA02009V1
21	64	3715961	PENCNOT09	961523H1 (BRSTTUT03), 1863723F6 (PROSNOT19), 2265329H1 (UTRSNOT02), 2360619R6 (LUNGFET05), 2360619T6 (LUNGFET05), 2821718H1 (ADRETUT06), 3715961H1 (PENCNOT09), 5016160H1 (BRAXNOT03), 5499583H1 (BRABDIR01)
22	65	5108194	PROSTUS19	1322651X35 (BLADNOT04), 1322651X36 (BLADNOT04), 3494841H1 (ADRETUT07), 4958978F6 (TLYMNOT05), 5108194H1 (PROSTUS19), g1379009, g1527417
23	66	5503122	BRABDIR01	5503122F6 (BRABDIR01), 5503122H1 (BRABDIR01), 5503122R6 (BRABDIR01)

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
24	67	5517972	LIVDIR01	805957R1 (BSTMT01), 953622R1 (SCORN01), 1501080F1 (SINTBST01), 1547381R6 (PROSTUT04), 2081843T6 (UTRSNOT08), 2811524F6 (OVARNOT10), 3212921H1 (BLADNOT08), 3250443H1 (SEMVN03), 3269479H1 (BRAINOT20), 3699955F6 (SININOT05), 3700568H1 (SININOT05), 4944050H1 (BRAIFEN05), 5517972H1 (LIVDIR01)
25	68	5593114	COLCDIT03	2859465F6 (SININOT03), 2859465T6 (SININOT03), 3555656F6 (LUNGNOT31), 3555656T6 (LUNGNOT31), 4345952H1 (TLYMTXT01), 5593114H1 (COLCDIT03), 5874544H1 (COLTDT04)
26	69	044775	TBLYN01	044775H1 (TBLYN01), 044775X3 (TBLYN01), 455640R1 (KERANOT01), 950702R1 (PANCNOT05), 2418550H1 (HNT3AZT01), 2798917H1 (NPOLNOT01), 2844696H1 (DRGLNOT01), g1718929
27	70	116588	KIDNNOT01	699714R6 (SYNORAT03), 831423R1 (PROSTUT04), 978875R1 (BRSTNOT02), 1350569F1 (LATRTUT02), 1447681R1 (PLACNOT02), 3177382F6 (UTRSTUT04), 3688796H1 (HEAANOT01), 3929008H1 (KIDNNOT19), g2106455, g2163092
28	71	875369	LUNGAST01	571573F1 (OVARNON01), 571573R1 (OVARNON01), 875369H1 (LUNGAST01), 875369R1 (LUNGAST01), 3569021H1 (HEAPNOT01)
29	72	1325518	LPARNOT02	1325518H1 (LPARNOT02), 1325518T6 (LPARNOT02), 1825553F6 (LSUBNOT03), SBAA02035F1
30	73	2060987	OVARNOT03	1378947T1 (LUNGNOT10), 1453290F1 (PENITUT01), 1459818R1 (COLNFET02), 1967477H1 (BRSTNOT04), 2060987H1 (OVARNOT03), 2455371F6 (ENDANOT01), 2499967F7 (ADRETUT05), 3093056T6 (BRSTNOT19), 3213366H1 (BLADNOT08), 4934158H1 (BRSTTUT20), SBYA01942U1
31	74	2172064	ENDCNOT03	2172064CT1 (ENDCNOT03), 2172064H1 (ENDCNOT03), SBAA01269F1
32	75	2219267	LUNGNOT18	2219267F6 (LUNGNOT18), 2219267H1 (LUNGNOT18), 3117478T6 (LUNGNOT13), 3126288T6 (LUNGNOT12), 3558495H1 (LUNGNOT31)
33	76	2308629	NGANNOT01	469862F1 (MMLR1DT01), 469862R1 (MMLR1DT01), 1594203X11C1 (BRAINOT14), 2191933H1 (THYRTUT03)
34	77	2660038	LUNGNOT09	1326594F1 (LPARNOT02), 2256143H1 (OVARNOT01), 2278689R6 (PROSNON01), 2528425H1 (GBLANOT02), 2660038H1 (LUNGNOT09), 2660038T6 (LUNGNOT09), 3449964H1 (UTRSNON03), 5099879H1 (PROSTUS20), g1886680, g783969

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
35	78	2670745	ESOGTUT02	259200X12 (HNT2RAT01), 1266477F1 (BRAINOT09), 2383364F6 (ISLTNOT01), 2670745H1 (ESOGTUT02), 3181526H1 (TLYJNOT01)
36	79	2676443	KIDNNOT19	607375R6 (BRSTTUT01), 1728626X15C1 (PROSNOT14), 1751773F6 (LIVRTUT01), 1751994T6 (LIVRTUT01), 1796032X14C1 (PROSTUT05), 2010172H1 (TESTNOT03), 2676443H1 (KIDNNOT19)
37	80	3295764	TLYJINT01	063264H1 (PLACNOB01), 434468T6 (THYRNOT01), 487721H1 (HNT2AGT01), 907796R2 (COLNNOT09), 1212556R7 (BRSTTUT01), 1251889H1 (LUNGFET03), 1653370F6 (PROSTUT08), 1653370X309D1 (PROSTUT08), 2192762F6 (THYRTUT03), 2226786F6 (SEMNOT01), 3295764H1 (TLYJINT01), 3384471H1 (ESOGNOT04), SASA01137F1
38	81	3438320	PENCNOT06	3438320H1 (PENCNOT06), 3501438H1 (PROSTUT13), 3745542H1 (THYMNOT08), 3751060H1 (UTRSNOT18), 4979750F6 (HELATXT04), SADA00043F1, SADA00087F1
39	82	3986488	UTRSTUT05	1634141F6 (COLNNOT19), 1692115X12C1 (PROSTUT10), 1731310F6 (BRSTTUT08), 2046232H1 (THP1T7T01), 3557951H1 (LUNGNOT31), 4726788H1 (GBLADIT01)
40	83	4378816	LUNGNOT37	1318962H1 (BLADNOT04), 1520864F1 (BLADTUT04), 1684381F6 (PROSNOT15), 2055747R6 (BEPINOT01), 4378816H1 (LUNGNOT37)
41	84	4797137	LIVRTUT09	4797137F6 (LIVRTUT09), 4797137H1 (LIVRTUT09), 4797137T6 (LIVRTUT09)
42	85	5470806	MCLRUNT01	5470806H1 (MCLRUNT01), 5470806T6 (MCLRUNT01)
43	86	5473242	MCLRUNT01	5473242F6 (MCLRUNT01), 5473242T6 (MCLRUNT01)

Table 2

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
1	623	S521 S2 T3 S16 S99 S138 S144 T193 T264 T404 S448 S589 S151 T229 T337 T457 S562 S568	N97 N333	BTB domain: C44-F56 POZ domain: N10-Q211 Kelch repeat signature: E379-G392, T398-V412, L438-M452, T498-A512 Ring canal protein repeat: E122-P254	Ring canal protein [Drosophila melanogaster] g577276	MOTIFS BLIMPS-PFAM BLIMPS-PRINTS BLAST-GenBank BLAST-PRODOM BLAST-DOMO
2	99	T17	N15	Signal peptide: M1-G36 Transmembrane region: S25-W45 MRP(2) MRP(1) repeat: C30-V74	Multi-drug resistance- associated protein (MRP)-like protein- 1 (MLP-1) [Rattus norvegicus] g3242458	MOTIFS BLAST-GenBank BLAST-PRODOM SPScan HMMER
3	374	T334 T33 S137 T146 S291 S311 T346	N103 N127 N135 N138	Signal peptide: M1-N52	Tricarboxylate carrier [Rattus sp.] g545998	MOTIFS BLAST-GenBank SPScan
4	271	S234 T126 T169 Y141		Signal peptide: M1-C30 Transmembrane region: L233-F252	Weak similarity with honeybee ATP synthase A chain [Caenorhabditis elegans] g3878801	MOTIFS BLAST-GenBank SPScan HMMER
5	323	S99 S125 S192 T277 S307 S309 T110 Y212		Leucine zipper: L284-L305	Cu ²⁺ -transporting ATPase homolog [Arabidopsis thaliana] g2464854	BLAST-GenBank MOTIFS
6	274	S96 T198 S215 T29 S121 S164 S170		Mitochondrial energy transfer proteins: G5-L266 Signal peptide: M1-G17	Pet8p [Saccharomyces cerevisiae] g495307	BLAST-GenBank HMMER-PFAM MOTIFS ProfileScan BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO SPScan

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
7	291	S6 T113 T173 T147 S230 T258	N226 N261	Signal peptide: M1-T42 Transmembrane domain: W29-I54 Band 7 protein family: C50-V62, K90-E224 Membrane stomatin: E14-N283	Stomatin [Homo sapiens] g1161562	MOTIFS BLAST-GenBank SPScan HMER BLIMPS-BLOCKS BLAST-DOMO BLAST-PRODOM
8	381	S2 S35 T57 S92 T104 S191 S302 S334 S335 S336 T43 T250 T255 T304 S311 S370 Y65	N218 N253 N259		K ⁺ channel modulatory factor DEBT-91 [Mus musculus] g4838557	MOTIFS BLAST-GenBank
9	190	T160 S17 T71 S77 T78 S111 S134 S142	N87	ABC transporter family: R79-K177 ATP/GTP-binding site motif A (P-loop): G102-S109	ABC2 transporter [Mus musculus] g495259	MOTIFS BLAST-GenBank BLAST-DOMO
10	297	S17 S114 T136 S16	N287	Mitochondrial carrier protein signature: E117-I297 Graves Disease carrier protein: P137-T157, L259-S279	Similar to human ADP/ATP carrier protein [C. elegans] g3879938	MOTIFS BLAST-GenBank HMER-PFAM BLIMPS-PRINTS
11	89	T37 T47 T60 S64			Mitochondrial import protein Tim9p [Saccharomyces cerevisiae] g3747026	BLAST-GenBank MOTIFS
12	115	T108 T84		Signal peptide: M1-G24 Transmembrane domain: G35-F57 Sodium neurotransmitter symporter signature: P7-S65		MOTIFS SPScan HMER ProfileScan

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SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
17	748	S55 S196 T254 S307 S327 T491 T534 T550 T571 S635 S648 S677 T696 S283 S291 T314 S629 S701 Y556	N531 N543 N548 N627	Signal peptide: M1-A61 Transmembrane domains: L39-L56, I167-F186, C229-F252, G438-L455, M492-F509, L598-I618 Ion transport proteins signature: F85-V251, L369-I618	Voltage-gated calcium channel [Rattus norvegicus] g4586963	BLAST-GenBank MOTIFS SPScan HMMER HMMER-PFAM BLIMPS-PRINTS
18	507	T200 S183 T232 T284 T349 T150 T252 S253 S319 S383 Y454	N220 N250 N364 N496	Signal peptide: M1-G26	Nucleoporin p54 [Rattus norvegicus] g1537070	BLAST-GenBank MOTIFS SPScan
19	592	S460 S104 T178 S320 S321 T498 T531 Y365		ABC1 precursor signature: N153-Q162, F210-A229, G234-I254, V312-G332, T366-V378	ABC transporter [Methanobacterium thermo.] g2622773	BLAST-GenBank MOTIFS BLIMPS-PRODOM BLAST-PRODOM
20	841	T98 S120 S203 T214 T276 S388 T438 T700 T838 T167 T179 S280 T370 S435 S531 S539 S666 S693 S830	N368 N490 N624	Transmembrane domains: Y451-D469, M544-F562, F577-F597, G775-W797 Vacuolar ion transport subunit signature: M10-F831	Vacuolar H ⁺ /ATPase subunit [Rattus norvegicus] g206430	BLAST-GenBank MOTIFS HMMER BLIMPS-PRODOM BLAST-PRODOM BLAST-DOMO
21	253	S50 T139 T152 T177 S202 T143 Y55		Mitochondrial carrier proteins domain: Y31-S248 Mitochondrial energy transfer proteins signature sequence: T62-Q96 T110-G122	Mitochondrial uncoupling protein UCP-4 [Homo sapiens] g4324701	BLAST-GenBank MOTIFS HMMER-PFAM BLIMPS-BLOCKS ProfileScan BLAST-PRODOM BLAST-DOMO

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
22	229	S69 S26 S109 T162 S178 S25 S64 S65 T210 S219		Signal peptide: M1-A47 Mitochondrial carrier proteins domain: Q32-G220 Mitochondrial carrier proteins signature sequence: S36-T49, T49-V63, G92-E112, T144-T162, Y187-F205	Grave's disease carrier protein [Bos taurus] g387	BLAST-GenBank MOTIFS SPScan HMMER-PFAM BLIMPS-BLOCKS ProfileScan BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO
23	170	S26 S31 S149 S164 T22 T157	N66 N145	Dihydroxyipyridine-sensitive L-type calcium channel signature: Y2-A47, I49-V77, A83-N100, R106-E131 SH3 domain: V59-R122	Voltage-dependent calcium channel beta-4 subunit [Homo sapiens] g2058727	BLAST-GenBank MOTIFS HMMER-PFAM BLIMPS-BLOCKS BLIMPS-PRINTS BLIMPS-PFAM BLAST-PRODOM BLAST-DOMO
24	655	T194 S195 S232 T362 S655 S4 S88 T135 T153 S187 T214 S322 T345 S353 S443 T609 S261 S381 S384	N338 N418 N557 N596	Transmembrane domains: I396-K417, Y494-S522, T538-V556 ABC transporters domain: P73-G262 ABC transporter family signature sequence: I78-L89, V186-D217	Breast cancer resistance protein (multidrug transporter) [Homo sapiens] g4038352	BLAST-GenBank MOTIFS HMMER HMMER-PFAM BLIMPS-BLOCKS ProfileScan BLAST-PRODOM BLAST-DOMO
25	184	T51 S29 T100 S138 S151 Y78	N27		Cation transport protein [E. coli] g495778	BLAST-GenBank MOTIFS
26	154	S54 S42 S62 T78 Y104		Mitochondrial energy transfer proteins signatures: P89-L97, M1-E41, M73-L152 Mitochondrial carrier protein domain: G2-L152	Similar to carrier protein C2 [C. elegans] g3879669	MOTIFS HMMER-PFAM BLAST-PRODOM BLAST-DOMO BLAST-GenBank

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
27	438	S170 T5 T51 T265 T300 S425	N50 N423	Transmembrane domains: C91-L111, L237-I257, I305-M332, M332-L354, L391-V408, I186-A204	Multidrug efflux transporter [Bacillus subtilis] g2635104	MOTIFS HMMER BLAST-GenBank
28	237	S10 S47 T72 S28 S96 S148 T173 T222 S6 S21 T32 T61 T192	N35	Nucleic acid-binding protein E5.1 domain: S6-K128	ARL-6 interacting protein-4 [Mus musculus] g4927204	MOTIFS BLAST-DOMO BLAST-GenBank
29	219	T66 S194 T200		Signal peptide: M1-R19 or M1-K15 Caseins alpha/beta signature: M1-N39	Surface antigen [Trypanosoma cruzi] g161956	MOTIFS HMMER SPScan ProfileScan BLAST-GenBank
30	707	S31 T6 T55 T263 T328 T546 T580 T594 S662 S673 T32 S50 S231 T244 T306 T385 S439 S476 S533 S553 S624	N343 N570 N638 N703	Potassium channel signature: A62-T81 Potassium channel integral membrane protein domain: S13-D117	NY-REN-45 antigen (similar to potassium channel protein) [Homo sapiens] g5360115	MOTIFS BLIMPS-PRINTS BLAST-DOMO BLAST-GenBank
31	279	T18 T245 T206	N181	Signal cleavage: M1-G45 Connexin domains: M1-V99, V20-Y44 Connexin signatures: L33-V86, L152-F205, F51-P73, S76-L96, L133-Y159, C169-T189, I190-L218 Gap junction protein connexin transmembrane regions: F5-Y97, L133- K223, M1-S130	Gap junction protein (similar to connexin) [Homo sapiens] g3006230	MOTIFS SPScan HMMER BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PFAM ProfileScan BLAST-PRODOM BLAST-DOMO BLAST-GenBank

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
32	154	S114		Signal peptide: M1-A35 or M1-A14 Transmembrane domain: F83-L102	mBOCT (potent organic cation transporter) [Mus musculus] g4589468	MOTIFS HMMER SPScan BLAST-GenBank
33	289	T83 T205 S269 T279	N60	Mitochondrial energy transfer proteins signatures: M1-G147, P17, P115, N185-K280, A101-Q181, Y184-I278 Mitochondrial carrier protein domains: M1-E176, N185-K280 Mitochondrial transmembrane transport protein regions: P17-R182, P180-I278	Mitochondrial solute carrier [Onchocerca volvulus] g1518458	MOTIFS HMMER-PFAM BLAST-DOMO BLAST-PRODOM ProfileScan BLAST-GenBank
34	300	S189 S195 S204 T257		Mitochondrial energy transfer proteins signatures: P19-M27, D2-I53, L209-L295 Mitochondrial carrier protein domain: D2-Y295 Transport protein domain: P122-Y295	YKL522=mitochondria 1 ADP/ATP carrier protein homolog [Saccharomyces cerevisiae] g254449	MOTIFS HMMER-PFAM ProfileScan BLAST-PRODOM BLAST-DOMO BLAST-GenBank
35	382	S34 S207 T221 S312 T40 S53 T112 T117 T277 S337	N96 N372	Keich motifs: H191-G249, E250-D301	Similarity to Human host cell factor C1 [Homo sapiens] g3875291	MOTIFS HMMER BLAST-PFAM BLAST-GenBank

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
36	287	T36 T118 S180 S230 T84 S168 T244		Mitochondrial energy transfer proteins signatures: P26-L34, P219-L227, L97-G193, W10-V89, D197-F281, P96-Y194 Mitochondrial carrier protein domain: A5-F281 Mitochondrial brown fat region: Y82-Q94, V151-S168, Y194-C212	Mitochondrial dicarboxylate carrier [Rattus norvegicus] g3646426	MOTIFS HMME-PFAM BLIMPS-PRINTS BLAST-DOMO BLAST-GenBank
37	497	T65 T135 S147 T360 S8 T22 S45 S291	N63 N314 N414	Transmembrane domains: M114-T137, M364-M380, Y390-A413, A421-D444, F456-V478 Folate transporter domains: W30-H218, I253-K484	Reduced folate carrier [Homo sapiens] g1041934	MOTIFS HMME BLAST-PRODOM BLAST-DOMO SPScan BLAST-GenBank
38	228	T21 S124 T145 S158 T190 T95 S132 S137 T177		Heme-binding domain in cytochrome b5: Y19-G98 Cytochrome b5 family domain: H28-P75	cytochrome b5 containing fusion protein [Helianthus annuus] g1040729 P=1.2e-07	MOTIFS HMME-PFAM BLAST-GenBank ProfileScan
39	273	T63 S158 T48	N214	Transmembrane domains: L85-N105, F180-Y200 Intermembrane space domain: L30-L251	Sqv-7-like protein (similar to nucleotide-sugar transporters) [Homo sapiens] g4008517	MOTIFS HMME BLAST-DOMO BLAST-GenBank

Table 2 (cont.)

SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs, and Domains	Homologous Sequences	Analytical Methods & Databases
40	206	S187 S201	N158	Signal peptide: M1-G29 or M1-A27 Emopamil binding protein: G37-S187, L15-K203 Transmembrane domain: Y164-L183	C-8,7 sterol isomerase, aSI1 [Arabidopsis thaliana] g2772934	MOTIFS HMMER ProfileScan BLAST-DOMO BLAST-GenBank
41	235	S192 S200 S56 T95 T146 S199 T207 S229 T53 T61 T69 T119 T148 Y70	N123	Transmembrane domain: F15-I34, M155-V174 Channel myelin protein: L18-M181 Sodium channel beta-2 subunit precursor: F15-E210 Immunoglobulin domain: I34-V136	Myelin protein zero (MPZ) [Homo sapiens] g2160399	MOTIFS HMMER BLIMPS-PRINTS BLAST-PRODUM BLAST-DOMO BLAST-GenBank
42	147	T79 T116 S3 S66 Y89 Y98	N118	Signal peptide: M1-G23 or M1-A20 Transthyretin signature: S28-S132 Transthyretin domain: G21-Q146	Transthyretin precursor [Sus scrofa] g1009702	MOTIFS HMMER ProfileScan BLAST-PRODUM BLAST-DOMO BLAST-GenBank BLIMPS-BLOCKS BLIMPS-PRINTS
43	147	T5 S88 T39		Globin domain: V2-H147 Heme oxygen transport protein domain: L32-H147	III beta-3 globin [Rattus norvegicus] g395943	MOTIFS HMMER-PFAM BLAST-PRODUM BLAST-DOMO BLIMPS-BLOCKS BLIMPS-PRINTS

Table 3

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
44	1567-1611 2107-2151	Gastrointestinal (0.203) Hematopoietic/Immune (0.188) Nervous (0.156)	Cell Proliferation and Cancer (0.547) Inflammation (0.422)	PBLUESCRIPT
45	1-92 351-434	Endocrine (0.333) Developmental (0.167) Gastrointestinal (0.167) Musculoskeletal (0.167) Reproductive (0.167)	Cell Proliferation and Cancer (0.833) Inflammation (0.167)	pINCY
46	920-964 1352-1396	Reproductive (0.304) Gastrointestinal (0.174) Cardiovascular (0.130) Hematopoietic/Immune (0.130) Nervous (0.130)	Cell Proliferation and Cancer (0.478) Inflammation (0.391)	PSPORT1
47	1-80 768-848	Nervous (0.273) Reproductive (0.273) Gastrointestinal (0.127) Hematopoietic/Immune (0.127)	Cell Proliferation and Cancer (0.564) Inflammation (0.400)	pINCY
48	111-194 687-758	Reproductive (0.221) Nervous (0.185) Gastrointestinal (0.124)	Cell Proliferation and Cancer (0.552) Inflammation (0.343)	pINCY
49	1-97	Nervous (0.234) Hematopoietic/Immune (0.191) Gastrointestinal (0.149)	Cell Proliferation and Cancer (0.617) Inflammation (0.340)	pINCY
50	218-262	Cardiovascular (1.000)	Cancer (0.333) Inflammation/Trauma (0.333) Cell Proliferation (0.333)	PSPORT1
51	811-855	Hematopoietic/Immune (0.180) Gastrointestinal (0.146) Reproductive (0.281)	Cancer (0.393) Inflammation/Trauma (0.515) Cell Proliferation (0.146)	PSPORT1
52	595-639	Gastrointestinal (0.286) Reproductive (0.714)	Cancer (0.429) Inflammation/Trauma (0.429)	pINCY
53	96-140	Cardiovascular (0.167) Hematopoietic/Immune (0.167) Nervous (0.250) Reproductive (0.167)	Cancer (0.250) Inflammation/Trauma (0.167) Cell Proliferation (0.167)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
54	507-551	Reproductive (0.323) Gastrointestinal (0.154) Nervous (0.123)	Cancer (0.446) Inflammation/Trauma (0.308) Cell Proliferation (0.185)	PBLUESCRIPT
55	455-499	Urologic (0.333) Nervous (0.222) Reproductive (0.222)	Cancer (0.667) Cell Proliferation (0.333)	PBLUESCRIPT
56	1835-1879	Nervous (0.625) Gastrointestinal (0.375)	Inflammation/Trauma (0.375) Cancer (0.250) Neurological (0.250)	pINCY
57	811-855	Gastrointestinal (1.000)	Inflammation/Trauma (0.667)	pINCY
58	390-434	Reproductive (0.320) Nervous (0.240) Urologic (0.120)	Cancer (0.520) Inflammation/Trauma (0.240) Cell Proliferation (0.160)	PSPORT1
59	413-457	Gastrointestinal (0.333) Musculoskeletal (0.333) Nervous (0.333)	Cancer (0.333) Neurological (0.333)	pINCY
60	2021-2084	Nervous (0.197) Gastrointestinal (0.184) Reproductive (0.184)	Cancer (0.461) Inflammation/Trauma (0.316) Cell Proliferation (0.118)	pINCY
61	65-109	Nervous (0.226) Reproductive (0.208) Cardiovascular (0.113) Gastrointestinal (0.113)	Cancer (0.528) Inflammation/Trauma (0.301) Cell Proliferation (0.208)	pINCY
62	379-423 1867-1911	Reproductive (0.282) Gastrointestinal (0.205) Nervous (0.154)	Cancer (0.538) Inflammation/Trauma (0.282) Cell Proliferation (0.103)	PSPORT1
63	362-406 1193-1237	Urologic (0.500) Reproductive (0.333) Cardiovascular (0.167)	Cancer (0.667) Inflammation/Trauma (0.333)	pINCY
64	394-438	Nervous (0.294) Reproductive (0.265) Cardiovascular (0.118)	Cancer (0.382) Inflammation/Trauma (0.235) Cell Proliferation (0.118)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
65	768-812	Reproductive (0.300) Endocrine (0.200) Gastrointestinal (0.200) Hematopoietic/Immune (0.200)	Inflammation/Trauma (0.500) Cancer (0.400)	pINCY
66	77-121	Nervous (1.000)	Neurological (1.000)	pINCY
67	1999-2043	Reproductive (0.324) Nervous (0.265) Gastrointestinal (0.235)	Cancer (0.500) Inflammation/Trauma (0.294) Cell Proliferation (0.118)	pINCY
68	561-605	Hematopoietic/Immune (0.455) Gastrointestinal (0.182) Nervous (0.182)	Inflammation/Trauma (0.546) Cell Proliferation (0.182)	pINCY
69	679-729	Nervous (0.292) Gastrointestinal (0.208) Hematopoietic/Immune (0.125)	Cancer (0.250) Cell Proliferation (0.375) Inflammation/Trauma (0.416)	PBLUESCRIPT
70	95-366 1078-1185	Reproductive (0.206) Hematopoietic/Immune (0.186) Cardiovascular (0.127)	Cancer (0.373) Inflammation/Trauma (0.382) Cell Proliferation (0.176)	PBLUESCRIPT
71	33-152	Reproductive (0.275) Nervous (0.163) Gastrointestinal (0.137)	Cancer (0.438) Inflammation/Trauma (0.314) Cell Proliferation (0.176)	PSPORT1
72	81-779	Gastrointestinal (1.000)	Cancer (1.000)	pINCY
73	719-817 1202-1414	Reproductive (0.311) Hematopoietic/Immune (0.203) Gastrointestinal (0.122)	Cancer (0.459) Inflammation/Trauma (0.379) Cell Proliferation (0.203)	PSPORT1
74	1-848	Nervous (0.750) Dermatologic (0.250)	Cancer (0.250) Cell Proliferation (0.250) Inflammation/Trauma (0.500)	pINCY
75	1-478	Cardiovascular (0.714) Developmental (0.143) Hematopoietic/Immune (0.143)	Cancer (0.571) Cell Proliferation (0.286) Inflammation (0.143)	pINCY
76	1-134	Reproductive (0.253) Nervous (0.241) Gastrointestinal (0.127) Hematopoietic (0.127)	Cancer (0.494) Inflammation (0.215) Cell Proliferation (0.127)	PSPORT1

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Table 3 (cont.)

Nucleotide SEQ ID NO:	Selected Fragments	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
77	510-719 960-1100	Reproductive (0.467) Cardiovascular (0.133) Gastrointestinal (0.133)	Cancer (0.467) Inflammation/Trauma (0.467)	pINCY
78	180-293	Reproductive (0.230) Nervous (0.225) Gastrointestinal (0.124)	Cancer (0.478) Inflammation/Trauma (0.292) Cell Proliferation (0.191)	pINCY
79	192-653 795-935	Reproductive (0.417) Gastrointestinal (0.292) Urologic (0.125)	Cancer (0.750) Cell Proliferation (0.125) Inflammation/Trauma (0.167)	pINCY
80	139-1044	Reproductive (0.245) Nervous (0.143) Developmental (0.122)	Cancer (0.490) Inflammation/Trauma (0.286) Cell Proliferation (0.224)	pINCY
81	233-916	Reproductive (0.667) Cardiovascular (0.167) Nervous (0.167)	Cancer (0.500) Cell Proliferation (0.333) Inflammation (0.167)	pINCY
82	1-153 760-816	Gastrointestinal (0.282) Hematopoietic/Immune (0.205) Reproductive (0.205)	Inflammation/Trauma (0.461) Cancer (0.308) Cell Proliferation (0.205)	pINCY
83	57-299	Nervous (0.179) Reproductive (0.179) Gastrointestinal (0.128)	Cancer (0.564) Cell Proliferation (0.256) Inflammation/Trauma (0.180)	pINCY
84	1-707	Gastrointestinal (0.500) Hematopoietic/Immune (0.500)	Cancer (0.500) Inflammation (0.500)	pINCY
85	451-594	Hematopoietic/Immune (1.000)	Cell Proliferation (1.000)	pINCY
86	8-124 161-187 407-472	Developmental (1.000)	Cell Proliferation (1.000)	pINCY

Table 4

SEQ ID NO:	Library	Library Comment
44	HNT2AGT01	Library was constructed at Stratagene (STR937233), using RNA isolated from the hNT2 cell line derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor. Cells were treated with retinoic acid for 5 weeks and with mitotic inhibitors for two weeks and allowed to mature for an additional 4 weeks in conditioned medium.
45	COLNFET02	Library was constructed using RNA isolated from the colon tissue of a Caucasian female fetus, who died at 20 weeks' gestation.
46	PANCNOT04	Library was constructed using RNA isolated from the pancreatic tissue of a 5-year-old Caucasian male, who died in a motor vehicle accident. Serology was positive for cytomegalovirus (CMV).
47	ADRETUT05	Library was constructed from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.
48	LUNGPUT11	Library was constructed using RNA isolated from lung tumor tissue removed from the right lower lobe of a 57-year-old Caucasian male during a segmental lung resection. Pathology indicated an infiltrating grade 4 squamous cell carcinoma. Multiple intrapulmonary peribronchial lymph nodes showed metastatic squamous cell carcinoma. Patient history included a benign brain neoplasm and tobacco abuse. Family history included spinal cord cancer, type II diabetes, cerebrovascular disease, and malignant prostate neoplasm.
49	BRAVXT03	Library was constructed using RNA isolated from treated astrocytes removed from the brain of a female fetus who died after 22 weeks' gestation. The cells were treated with tumor necrosis factor (TNF) alpha and interleukin 1 (IL-1), 10ng/ml each for 24 hours.
50	LUNGAST01	Library was constructed using RNA isolated from the lung tissue of a 17-year-old Caucasian male, who died from head trauma. Patient history included asthma.
51	OVARNOT02	Library was constructed using RNA isolated from ovarian tissue removed from a 59-year-old Caucasian female who died of a myocardial infarction. Patient history included cardiomyopathy, coronary artery disease, previous myocardial infarctions, hypercholesterolemia, hypotension, and arthritis.
52	BRSTNOT13	Library was constructed using RNA isolated from breast tissue removed from the left medial lateral breast of a 36-year-old Caucasian female during bilateral simple mastectomy and total breast reconstruction. Pathology indicated benign breast tissue. Patient history included a breast neoplasm, depressive disorder, hyperlipidemia, chronic stomach ulcer, and an ectopic pregnancy. Family history included myocardial infarction, cerebrovascular disease, atherosclerotic coronary artery disease, hyperlipidemia, skin cancer, breast cancer, depressive disorder, esophageal cancer, bone cancer, Hodgkin's lymphoma, bladder cancer, and a heart condition.

Table 4 (cont.)

SEQ ID NO:	Library	Library Comment
53	SMCCNOS01	Library was constructed using 7.56 X 10 ⁶ clones from a coronary artery smooth muscle cell library and was subjected to two rounds of subtraction hybridization for 48 hours with 6.12 X 10 ⁶ clones from a control coronary artery smooth muscle cell library. The starting library for subtraction was constructed using RNA isolated from coronary artery smooth muscle cells removed from a 3-year-old Caucasian male. The cells were treated with TNF alpha & IL-1 beta 10ng/ml each for 20 hours. The hybridization probe for subtraction was derived from a similarly constructed library from RNA isolated from untreated coronary artery smooth muscle cells from the same donor.
54	HUVENOB01	Library was constructed using RNA isolated from HUV-EC-C (ATCC CRL 1730) cells.
55	HNT2RAT01	Library was constructed at Stratagene (STR937231), using RNA isolated from the hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor). Cells were treated with retinoic acid for 24 hours.
56	SINTBST01	Library was constructed using RNA isolated from ileum tissue obtained from an 18-year-old Caucasian female during bowel anastomosis. Pathology indicated Crohn's disease of the ileum, involving 15 cm of the small bowel. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
57	ISLTNOT01	Library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.
58	COLNNOT11	Library was constructed using RNA isolated from colon tissue removed from a 60-year-old Caucasian male during a left hemicolectomy.
59	BONRTUT01	Library was constructed using RNA isolated from rib tumor tissue removed from a 16-year-old Caucasian male during a rib osteotomy and a wedge resection of the lung. Pathology indicated metastatic grade 3 (of 4) osteosarcoma, forming a mass involving the chest wall.
60	LUNGTTUT10	Library was constructed using RNA isolated from lung tumor tissue removed from the left upper lobe of a 65-year-old Caucasian female during a segmental lung resection. Pathology indicated metastatic grade 2 myxoid liposarcoma and metastatic grade 4 liposarcoma. Patient history included soft tissue cancer, breast cancer, and secondary lung cancer.
61	OVARNOT09	Library was constructed using RNA isolated from ovarian tissue removed from a 28-year-old Caucasian female during a vaginal hysterectomy and removal of the fallopian tubes and ovaries. Pathology indicated multiple follicular cysts ranging in size from 0.4 to 1.5 cm in the right and left ovaries, chronic cervicitis and squamous metaplasia of the cervix, and endometrium in weakly proliferative phase. Family history included benign hypertension, hyperlipidemia, and atherosclerotic coronary artery disease.

Table 4 (cont.)

SEQ ID NO:	Library	Library Comment
62	THPIAZS08	Library was constructed using 5.76 million clones from a 5-aza-2'-deoxycytidine (AZ) treated THP-1 promonocyte cell line library. Starting RNA was made from THP-1 promonocyte cells treated for three days with 0.8 micromolar AZ. 5.76 million clones from the AZ-treated THP-1 cell library were then subjected to two rounds of subtractive hybridization with 5 million clones from the untreated THP-1 cell library. Subtractive hybridization conditions were based on the methodologies of Swaroop et al. (1991) Nucleic Acids Res. 19:1954, and Bonaldo et al. (1996) Genome Research 6:791. THP-1 (ATCC TIB 202) is a human promonocyte cell line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia (ref: Int. J. Cancer (1980) 26:171).
63	BRSTNOT12	Library was constructed using RNA isolated from diseased breast tissue removed from a 32-year-old Caucasian female during a bilateral reduction mammoplasty. Pathology indicated nonproliferative fibrocystic disease. Family history included benign hypertension and atherosclerotic coronary artery disease.
64	PENCNOT09	Library was constructed using RNA isolated from penis right corpora cavernosa tissue.
65	PROSTUS19	Library was constructed using 2.36 million clones from a prostate tumor library which was subjected to two rounds of subtraction hybridization with 2.36 million clones from a normal prostate library. The starting library for subtraction was constructed using RNA isolated from prostate tumor tissue removed from a 59-year-old Caucasian male during a radical prostatectomy with regional lymph node excision. Pathology indicated adenocarcinoma (Gleason grade 3+3) involving the prostate peripherally with invasion of the capsule. Adenofibromatous hyperplasia was present. The patient presented with elevated prostate-specific antigen (PSA). Patient history included diverticulitis of the colon, asbestosis, and thrombophlebitis. Family history included benign hypertension, multiple myeloma, hyperlipidemia, and rheumatoid arthritis. The hybridization probe for subtraction was derived from a similarly constructed library, except that NotI-anchored oligo(dT) primer was used. Subtractive hybridization conditions were based on the methodologies of Swaroop et al. (1991) Nucleic Acids Res. 19:1954 and Bonaldo, et al. (1996) Genome Research 6:791.
66	BRABDIR01	Library was constructed using RNA isolated from diseased cerebellum tissue removed from the brain of a 57-year-old Caucasian male, who died from a cerebrovascular accident. Patient history included Huntington's disease, emphysema, and tobacco abuse.
67	LIVRDIR01	Library was constructed using RNA isolated from diseased liver tissue removed from a 63-year-old Caucasian female during a liver transplant. Patient history included primary biliary cirrhosis. Serology was positive for anti-mitochondrial antibody.

Table 4 (cont.)

SEQ ID NO:	Library	Library Comment
68	COLCDIT03	Library was constructed using RNA isolated from diseased colon polyp tissue removed from the cecum of a 67-year-old female. Pathology indicated a benign cecum polyp. Pathology for the associated tumor tissue indicated invasive grade 3 adenocarcinoma that arose in tubulovillous adenoma forming a fungating mass in the cecum.
69	TBLYNOT01	Library was constructed at Stratagene (STR937214) using RNA isolated from a hybrid of T-B lymphoblasts from an untreated leukemic cell line.
70	KIDNNOT01	Library was constructed using RNA isolated from the kidney tissue of a 64-year-old Caucasian female, who died from an intracranial bleed. Patient history included rheumatoid arthritis and tobacco use.
71	LUNGAST01	Library was constructed using RNA isolated from the lung tissue of a 17-year-old Caucasian male, who died from head trauma. Patient history included asthma.
72	LPARNOT02	Library was constructed using RNA isolated from tissue obtained from the left parotid (salivary) gland of a 70-year-old male with parotid cancer.
73	OVARNOT03	Library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during a bilateral salpingo-oophorectomy. Pathology for the associated tumor tissue indicated grade 2 mucinous cyst adenocarcinoma. The patient presented with stress incontinence. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, cerebrovascular disease, breast cancer, and uterine cancer.
74	ENDCNOT03	Library was constructed using RNA isolated from dermal microvascular endothelial cells removed from a neonatal Caucasian male.
75	LUNGNOT18	Library was constructed using RNA isolated from left upper lobe lung tissue removed from a 66-year-old Caucasian female. Pathology for the associated tumor tissue indicated a grade 2 adenocarcinoma. Patient history included cerebrovascular disease, atherosclerotic coronary artery disease, and pulmonary insufficiency. Family history included a myocardial infarction and atherosclerotic coronary artery disease.
76	NGANNOT01	Library was constructed using RNA isolated from tumorous neuroganglion tissue removed from a 9-year-old Caucasian male during a soft tissue excision of the chest wall. Pathology indicated a ganglioneuroma. Family history included asthma.
77	LUNGUT09	Library was constructed using RNA isolated from lung tumor tissue removed from a 68-year-old Caucasian male during segmental lung resection. Pathology indicated invasive grade 3 squamous cell carcinoma and a metastatic tumor. Patient history included type II diabetes, thyroid disorder, depressive disorder, hyperlipidemia, esophageal ulcer, and tobacco use.

Table 4 (cont.)

SEQ ID NO:	Library	Library Comment
78	ESOGTUT02	Library was constructed using RNA isolated from esophageal tumor tissue obtained from a 61-year-old Caucasian male during a partial esophagectomy, proximal gastrectomy, pyloromyotomy, and regional lymph node excision. Pathology indicated an invasive grade 3 adenocarcinoma in the esophagus. Family history included atherosclerotic coronary artery disease, type II diabetes, chronic liver disease, primary cardiomyopathy, benign hypertension, and cerebrovascular disease.
79	KIDNNOT19	Library was constructed using RNA isolated from kidney tissue removed a 65-year-old Caucasian male during an exploratory laparotomy and nephroureterectomy. Pathology for the associated tumor tissue indicated a grade 1 renal cell carcinoma within the upper pole of the left kidney. Patient history included malignant melanoma of the abdominal skin, benign neoplasm of colon, cerebrovascular disease, and umbilical hernia. Family history included myocardial infarction, atherosclerotic coronary artery disease, cerebrovascular disease, and prostate cancer.
80	TLYJINT01	Library was constructed using RNA isolated from a Jurkat cell line derived from the T cells of a male. Patient history included acute T-cell leukemia. This is an uninduced Jurkat cell line library from the same donor.
81	PENCNOT06	Library was constructed using RNA isolated from penis corpora cavernosa tissue removed from a 3-year-old Black male. Pathology for the associated tumor tissue indicated invasive grade 4 urothelial carcinoma forming a soft tissue scrotal mass that invaded the cavernous body of the penis and encased both testicles. Right inguinal lymph node showed metastatic grade 4 urothelial carcinoma, with extranodal invasion.
82	UTRSTUT05	Library was constructed using RNA isolated from uterine tumor tissue removed from a 41-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. Pathology indicated uterine leiomyoma. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Patient history included a ventral hernia and a benign ovarian neoplasm.
83	LUNGNOT37	Library was constructed using polyA RNA isolated from lung tissue removed from a 15-year-old Caucasian female who died from a closed head injury. Serology was positive for cytomegalovirus.
84	LIVRTUT09	Library was constructed using RNA isolated from an untreated C3A hepatocyte cell line which is a derivative of Hep G2, a cell line derived from a hepatoblastoma removed from a 15-year-old Caucasian male.
85	MCLRUNT01	Library was constructed using RNA isolated from untreated peripheral blood mononuclear cell tissue obtained from buffy coat, removed from a 60-year-old male.
86	MCLRUNT01	Library was constructed using RNA isolated from untreated peripheral blood mononuclear cell tissue obtained from buffy coat, removed from a 60-year-old male.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	PE Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	PE Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	PE Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	